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JUN 25 2001

TECH CENTER 1600/2900

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#9  
Dm  
8-37  
165281

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/668,788

DATE: 06/01/2001

TIME: 10:43:01

Input Set : A:\seqlist.txt

Output Set: C:\CRF3\06012001\I668788.raw

ENTERED

and 4 <110> APPLICANT: GVS Gesellschaft Fur Erwerb und Verwertung von Schutzrechten-GVS mbH

5       Forschungszentrum Borstel  
6       Wolter, Frank P.  
7       Jorasch, Petra  
8       Heinz, Ernst  
9       Zahringer, Ulrich  
12 <120> TITLE OF INVENTION: Processive Sugar Transferase  
15 <130> FILE REFERENCE: MAIWAM2.001CP1  
17 <140> CURRENT APPLICATION NUMBER: US 09/668,788  
18 <141> CURRENT FILING DATE: 2000-09-22  
20 <150> PRIOR APPLICATION NUMBER: PCT/DE99/00857  
21 <151> PRIOR FILING DATE: 1999-03-25  
23 <150> PRIOR APPLICATION NUMBER: DE 198 13 017.1  
24 <151> PRIOR FILING DATE: 1998-03-25  
26 <150> PRIOR APPLICATION NUMBER: DE 198 19 958.9  
27 <151> PRIOR FILING DATE: 1998-05-05  
29 <160> NUMBER OF SEQ ID NOS: 4  
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
33 <210> SEQ ID NO: 1  
34 <211> LENGTH: 1149  
35 <212> TYPE: DNA  
36 <213> ORGANISM: Bacillus subtilis  
38 <400> SEQUENCE: 1  
39 ttgaatacca ataaaagagt attaatTTTg actgcaaatt acggaaatgg acatgtgcag 60  
40 gtagccaaaa cactttatga acaatgtgta cggctcggct ttcagcatgt aacagtttct 120  
41 aatttgTacc aagagtcaaa tccgattgtt tcagaggtaa ctcaatacct ttatttAAAA 180  
42 agctttctcaa tcgggaaaca gttttatcgt ttgttttatt acggagttga caaaatctat 240  
43 aataaacgta aattcaatat ttacttttaa atgggtaata aaagattggg cgaacttgTc 300  
44 gatgaacatc agcccgatat tattattaat acatttccga tgatcgTcgt gccggaatac 360  
45 agacgccgaa ctggaagagt cattcctacc ttcaacgTta tgactgattt ttgtcttcat 420  
46 aaaatttggg ttcacgaaaa cgtggataaa tattatgtgg cgacagatta cgtgaaggaa 480  
47 aaactgctgg agatcggcac tcatccaagc aatgtaaaaa tcacaggaat tccaatcagg 540  
48 ccgcaatttg aagaatccat gcctgtttgg ccgatataata aaaagtacaa tctttcacca 600  
49 aacaaaaaag tgcttctgat catggcaggt gtcacaggTg tattaagaa cgtaaaagag 660  
50 ctgtgcgaaa accttgTcaa ggatgaccaa gtgcaagtag ttgtcgtgtg cgggaaaaat 720  
51 acggctttta aagaatcttt gagtgcgctt gaagcggaaa atggtgacaa attaaaagtt 780  
52 ctgggctatg tggagcgcat tgatgagcta tttcggatca cagattgcat gattaccaag 840  
53 cccggcggca ttactttgac agaagccaca gccattggag tgcctgtcat tctgtacaaa 900  
54 cccgtgcctg gccaggaaaa agaaaatgca aacttctttg aagaccgagg agctgccatc 960  
55 gttgtgaacc gtcatgaaga gattctcgag tcagtcactt cccttcttgc agatgaagat 1020  
56 accttgcatc gcatgaagaa aaacattaag gaccttcatt tagcaaactc ctctgaagtg 1080  
57 attttagagg atatcctgaa ggaatcagaa atgatgaccg ccaaacaaaa agccaaagtg 1140  
58 ctatcgtaa 1149  
60 <210> SEQ ID NO: 2  
61 <211> LENGTH: 382  
62 <212> TYPE: PRT  
63 <213> ORGANISM: Bacillus subtilis

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65 &lt;400&gt; SEQUENCE: 2

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66 Met Asn Thr Asn Lys Arg Val Leu Ile Leu Thr Ala Asn Tyr Gly Asn
67 1 5 10 15
68 Gly His Val Gln Val Ala Lys Thr Leu Tyr Glu Gln Cys Val Arg Leu
69 20 25 30
70 Gly Phe Gln His Val Thr Val Ser Asn Leu Tyr Gln Glu Ser Asn Pro
71 35 40 45
72 Ile Val Ser Glu Val Thr Gln Tyr Leu Tyr Leu Lys Ser Phe Ser Ile
73 50 55 60
74 Gly Lys Gln Phe Tyr Arg Leu Phe Tyr Tyr Gly Val Asp Lys Ile Tyr
75 65 70 75 80
76 Asn Lys Arg Lys Phe Asn Ile Tyr Phe Lys Met Gly Asn Lys Arg Leu
77 85 90 95
78 Gly Glu Leu Val Asp Glu His Gln Pro Asp Ile Ile Ile Asn Thr Phe
79 100 105 110
80 Pro Met Ile Val Val Pro Glu Tyr Arg Arg Arg Thr Gly Arg Val Ile
81 115 120 125
82 Pro Thr Phe Asn Val Met Thr Asp Phe Cys Leu His Lys Ile Trp Val
83 130 135 140
84 His Glu Asn Val Asp Lys Tyr Tyr Val Ala Thr Asp Tyr Val Lys Glu
85 145 150 155 160
86 Lys Leu Leu Glu Ile Gly Thr His Pro Ser Asn Val Lys Ile Thr Gly
87 165 170 175
88 Ile Pro Ile Arg Pro Gln Phe Glu Glu Ser Met Pro Val Gly Pro Ile
89 180 185 190
90 Tyr Lys Lys Tyr Asn Leu Ser Pro Asn Lys Lys Val Leu Leu Ile Met
91 195 200 205
92 Ala Gly Ala His Gly Val Leu Lys Asn Val Lys Glu Leu Cys Glu Asn
93 210 215 220
94 Leu Val Lys Asp Asp Gln Val Gln Val Val Val Val Cys Gly Lys Asn
95 225 230 235 240
96 Thr Ala Leu Lys Glu Ser Leu Ser Ala Leu Glu Ala Glu Asn Gly Asp
97 245 250 255
98 Lys Leu Lys Val Leu Gly Tyr Val Glu Arg Ile Asp Glu Leu Phe Arg
99 260 265 270
100 Ile Thr Asp Cys Met Ile Thr Lys Pro Gly Gly Ile Thr Leu Thr Glu
101 275 280 285
102 Ala Thr Ala Ile Gly Val Pro Val Ile Leu Tyr Lys Pro Val Pro Gly
103 290 295 300
104 Gln Glu Lys Glu Asn Ala Asn Phe Phe Glu Asp Arg Gly Ala Ala Ile
105 305 310 315 320
106 Val Val Asn Arg His Glu Glu Ile Leu Glu Ser Val Thr Ser Leu Leu
107 325 330 335
108 Ala Asp Glu Asp Thr Leu His Arg Met Lys Lys Asn Ile Lys Asp Leu
109 340 345 350
110 His Leu Ala Asn Ser Ser Glu Val Ile Leu Glu Asp Ile Leu Lys Glu
111 355 360 365
112 Ser Glu Met Met Thr Ala Lys Gln Lys Ala Lys Val Leu Ser
113 370 375 380

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116 <210> SEQ ID NO: 3
117 <211> LENGTH: 975
118 <212> TYPE: DNA
119 <213> ORGANISM: Staphylococcus aureus
121 <400> SEQUENCE: 3
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123 caagttacac agagtatcgt taatcaactt aatgatatga atctagacca tttaagcgtc 120
124 attgagcacg atttatttat ggaagctcat ccaattttga cttctatttg taaaaaatgg 180
125 tatatcaata gcttttaata ttttagaaat atgtacaaag ggttttatta cagccgcca 240
126 gataaactag acaaatgttt ttacaaatac tatggactta ataagttaat taatttattg 300
127 ataaaagaaa agccagattt aatattatta acgtttccta caccagttat gtcggtacta 360
128 actgagcaat ttaacattaa tattccagtt gctacagtga tgacagacta tcgcttacat 420
129 aaaaactgga ttacgccgta ttcaacaaga tattatgtgg caacaaaaga aacgaaacaa 480
130 gacttcatag acgtaggtat tgatccttca acagttaaag tgacaggtat tcctattgat 540
131 aacaaatttg aaacgcctat taatcaaaag cagtgggttaa tagacaacaa cttagatcca 600
132 gataagcaaa ctattttaat gtcagctggt gcatttggtg tatctaaagg ttttgacacg 660
133 atgattactg atatattagc gaaaagtgc aatgcacaag tagttatgat ttgtggttaag 720
134 agcaaagagc taaagcgttc tttaacagct aagtttaaat taacgagaat gtatttgatt 780
135 ctaggttata ccaaacacat gaatgaatgg atggcatcaa gtcaacttat gattacgaaa 840
136 cctggtggtg tcacaataac tgaaggtttc gcccgttgta ttccaatgat tttcctaaat 900
137 cctgcacctg gtcaagagct tgaaaatgcc ttttactttg aagaaaaagg ttttggtaaa 960
138 acgctgatac tccag                                     975

140 <210> SEQ ID NO: 4
141 <211> LENGTH: 391
142 <212> TYPE: PRT
143 <213> ORGANISM: Staphylococcus aureus
145 <400> SEQUENCE: 4
146 Met Val Thr Gln Asn Lys Lys Ile Leu Ile Ile Thr Gly Ser Phe Gly
147 1 5 10 15
148 Asn Gly His Met Gln Val Thr Gln Ser Ile Val Asn Gln Leu Asn Asp
149 20 25 30
150 Met Asn Leu Asp His Leu Ser Val Ile Glu His Asp Leu Phe Met Glu
151 35 40 45
152 Ala His Pro Ile Leu Thr Ser Ile Cys Lys Lys Trp Tyr Ile Asn Ser
153 50 55 60
154 Phe Lys Tyr Phe Arg Asn Met Tyr Lys Gly Phe Tyr Tyr Ser Arg Pro
155 65 70 75 80
156 Asp Lys Leu Asp Lys Cys Phe Tyr Lys Tyr Tyr Gly Leu Asn Lys Leu
157 85 90 95
158 Ile Asn Leu Leu Ile Lys Glu Lys Pro Asp Leu Ile Leu Leu Thr Phe
159 100 105 110
160 Pro Thr Pro Val Met Ser Val Leu Thr Glu Gln Phe Asn Ile Asn Ile
161 115 120 125
162 Pro Val Ala Thr Val Met Thr Asp Tyr Arg Leu His Lys Asn Trp Ile
163 130 135 140
164 Thr Pro Tyr Ser Thr Arg Tyr Tyr Val Ala Thr Lys Glu Thr Lys Gln
165 145 150 155 160
166 Asp Phe Ile Asp Val Gly Ile Asp Pro Ser Thr Val Lys Val Thr Gly
167 165 170 175

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```

168 Ile Pro Ile Asp Asn Lys Phe Glu Thr Pro Ile Asn Gln Lys Gln Trp
169      180      185      190
170 Leu Ile Asp Asn Asn Leu Asp Pro Asp Lys Gln Thr Ile Leu Met Ser
171      195      200      205
172 Ala Gly Ala Phe Gly Val Ser Lys Gly Phe Asp Thr Met Ile Thr Asp
173      210      215      220
174 Ile Leu Ala Lys Ser Ala Asn Ala Gln Val Val Met Ile Cys Gly Lys
175 225      230      235      240
176 Ser Lys Glu Leu Lys Arg Ser Leu Thr Ala Lys Phe Lys Leu Thr Arg
177      245      250      255
178 Met Tyr Leu Ile Leu Gly Tyr Thr Lys His Met Asn Glu Trp Met Ala
179      260      265      270
180 Ser Ser Gln Leu Met Ile Thr Lys Pro Gly Gly Ile Thr Ile Thr Glu
181      275      280      285
182 Gly Phe Ala Arg Cys Ile Pro Met Ile Phe Leu Asn Pro Ala Pro Gly
183      290      295      300
184 Gln Glu Leu Glu Asn Ala Phe Tyr Phe Glu Glu Lys Gly Phe Gly Lys
185 305      310      315      320
186 Ile Ala Asp Thr Pro Glu Glu Ala Ile Lys Ile Val Ala Ser Leu Thr
187      325      330      335
188 Asn Gly Asn Glu Gln Leu Thr Asn Met Ile Ser Thr Met Glu Gln Asp
189      340      345      350
190 Lys Ile Lys Tyr Ala Thr Gln Thr Ile Cys Arg Asp Leu Leu Asp Leu
191      355      360      365
192 Ile Gly His Ser Ser Gln Pro Gln Glu Ile Tyr Gly Lys Val Pro Leu
193      370      375      380
194 Tyr Ala Arg Phe Phe Val Lys
195 385      390

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VERIFICATION SUMMARY

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